WO 2005/092917 PCT/CA2004/000443

## SEQUENCE LISTING

<110> Wei, Xin Gariepy , Jean

<120> LIBRARY OF TOXIN MUTANTS, AND METHODS OF USING SAME

<130> 34104-0082

<160> 7

<170> PatentIn version 3.2

<210> .1

<211>. 299

<212> PRT

<213> Escherichia coli

<220>

<221> misc\_feature

<223> Wild type SLT-1 A chain

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35 40 45

Ser Gly Ser Gly Asp Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp 50 60

Pro Glu Glu Gly Arg Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn 65 70 75 80

Asn Leu Tyr Val. Thr Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr 90 95

Arg Phe Ala Asp Phe Ser His Val Thr Phe Pro Gly Thr Tar Ala Val

Thr Leu Ser Gly Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly
115 120 125

Ile Ser Arg Thr Gly Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser

1yr 145	Leu	Asp	ren.	wec	150	His	ser	GTĀ	Thr	155	ren	Thr	Gin	Ser	Val 160		·	
A1a	Arg	Ala	Met	Leu 165	Ārg	Phe	Val	Thr	Val 170	Thr	Ala	Glu	Ма	Leu 175	Arg		•	
Phe	Arg	Gln	Ile 180	Gln	Arg	GJA	Phe	Arg 185	.Thr	Thr	Len	Asp	1.8p	Leu	ser			
Gly	Arg	Ser 195	Tyr	Val	Met	Thr	Ala 200	Glu	Asp	Val	Asp	Leu 205	7'hr	Leu	Asn	•	·	-
Trp	Giy 210	Arg	Leu	Ser	Ser	Val. 215	Leu	Pro	Asp	Tyr	320 His	_	Gln	Asp.	Ser			
val 225	Arg	Va1	GŢĀ	Arg	I1e 230	Ser	Phe	Gly	Ser	Ile 235	Asn	Ala	Tle	Leu	Gly 240			
Ser	Val	Ala	Leu	Ile 245		neA	Cys	Hiş	His 250		Ala	Ser	<i>}</i> _g	Val 255	Ala			
Arg	Met	Ala	Ser 260		Glu	Phe	Pro	Ser 265		Суs	Pro	Ala	. ?.sp 270		'Arg			
Val	Arg	275		Thr	His	Asn	Lys 280		Leu	Trp	Asr	Ser 285	•	Thr	. Per		•	
Gly	Ala 290		Lev	Met	: Arg	Arg 295		: Ile	e Ser	: Ser	<del>,</del>			٠				
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	20> 23>	Pri	mer					•	,									•

31

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Val	Asp	Ser 35	Leu	Asn	Val	Ile	arg 40	Ser	Ala	Ile	Glyr	Thr 45	Fro	Leu	Gln
Thr	Ile 50	Ser	Ser	Gly	Gly	Thr 55	Ser	Leu	Leu	Mec	Ile 60	Asp	; er	Gly	Ser
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Asp	Phe	Ser 115		Val	Thr	Phe	Pro 120	ĠĮŻ	Thr	Thr	Ala	Val 125		Leu	Ser
Gly	7 Asp 130		· Ser	TYX	Thr	Thr 135	Leu	Glņ	Arg	Val	Ale: 140	_	lle	. Ser	<b>A</b> xg
Thr 145	_	r Met	Gln	Ile	Asn 150	Arg	His	Ser	Leu	Thr 155		ser ser	Jyr	Leu	Asp 160
Lev	ı Met	: Sei	His	Ser 165		Thr	Ser	Leu	Thr 170		ı Ser	· Val	L Ala	a Arg 175	Ala

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180

185

3.90

Ile Gln Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser (ly Arg Ser 195 200 205

Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg 210 215 220

Leu Ser Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val 225 230 235 240

Gly Arg Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala 245 250 255

Leu Ile Leu Asn Cys His His His Ile Tyr Ser Asn Lys Leu Met Ala 260 265 270

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Val Asp Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Fro Leu Gln
35 40 45

Thr Ile Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Ser 50 55

Gly Asp Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp Fro Glu Glu 65 70 75 80

Gly Arg Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr 85 90 95

- Val Thr Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala 100 105 3.10
- Asp Phe Ser His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser 115 120 125
- Gly Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ele Ser Arg 130 135 140
- Thr Gly Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp 145 150 150
- Leu Met Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val 3.la Arg Ala 165 170 175
- Met Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg Fhe Arg Gln
  180 185 190
- Ile Gln Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Cly Arg Ser 195 200 205
- Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg 210 215 220
- Leu Ser Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val 225 230 240
- Gly Arg Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala 245 250 255
- Leu Ile Leu Asn Cys His His His Ala Ala Phe Ala Asp Ieu Ile Ala 260 265 270
- Ser Arg Val Ala Arg Met Ala Ser Asp Glu Phe Pro Ser Met Cys Pro 275 280 285
- Ala Asp Gly Arg Val Arg Gly Ile Thr His Asn Lys Ile Leu Trp Asp 290 295 300
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